

SEQ ID NO:1

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc
121 ggcgaaaagga agcggctgag gcgcttgga cccgaaaagt ctccgtgctc ctggctacct
181 cgcacagcgg tgcccgcgg gccgtcagta ccatggacag cagcgtgccc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgact caagttgctc cccagcacc ccccccgggt
301 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcggt ccgaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtccctcc atgatcacgg
421 ccatcacgat catggccctc tactccatcg tgtgcgtgg ggggctcttc ggaaacttcc
481 tggatcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtaccct gcccttccag agtgtgaatt
601 acctaatggg aacatggcca tttggaacca tcctttgcaa gatagtgat tccatagatt
661 actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacattg
721 cagtctgcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaa ctggatcctc tcttcagcca ttggtcttcc tgtaatgttc atggctacaa
841 caaaatacag gcaaggttcc atagattgta cactaacatt ctctcatcca acctgggtact
901 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgccg gtgctcatca
961 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcatg ctctctgggt
1021 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctgggt gtgggtggctg
1081 tgttcacgtg ctgctggact cccattcaca tttacgtcat cattaagacc ttggttacaa
1141 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgctcta ggttacacaa
1201 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgaatgcttc
1261 gagagttctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaacactag agaccacccc tccacggcca atacagtggg tagaactaat catcagctag
1381 aaaatctgga agcagaaact gctccgttgc cctaacaggg tctcatgcc ttcgacctt
1441 caccaagctt agaagccacc atgtatgtgg aagcaggttg cttcaagaat gtgtaggagg
1501 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
1561 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttggg aggaaaggaa
1621 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaacaaa acccatcgtg
1681 gtatgtgaat tgaagtcatc ataaaagggt acccttctgt ctgtaagatt ttattttcaa
1741 gcaaatatth atgacctcaa caaagaagaa ccactttttg ttaagttcac cgtagtaaca
1801 cataaagtaa atgctacctc tgatcaaagc acctggaatg gaaggtccga gtctttttag
1861 tgtttttgca agggaaatgaa tccattattc tatttttagac ttttaacttc aacttaaaat
1921 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1981 aataacatct ctttcatcta gctccataat tgcaagggaa gagattagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaatactt
2101 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtgggttg ttcttggaa
2161 tc

FIGURE 1B

SEO ID NO:2

Met	Asp	Ser	Ser	Ala	Ala	Pro	Thr	Asn	Ala	Ser	Asn	Cys	Thr	Asp	Ala
1				5					10					15	
Leu	Ala	Tyr	Ser	Ser	Cys	Ser	Pro	Ala	Pro	Ser	Pro	Gly	Ser	Trp	Val
			20					25					30		
Asn	Leu	Ser	His	Leu	Asp	Gly	Asn	Leu	Ser	Asp	Pro	Cys	Gly	Pro	Asn
		35				40					45				
Arg	Thr	Asn	Leu	Gly	Gly	Arg	Asp	Ser	Leu	Cys	Pro	Pro	Thr	Gly	Ser
	50				55					60					
Pro	Ser	Met	Ile	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val
65				70					75					80	
Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val
				85				90						95	
Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu
		100					105					110			
Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val
		115				120					125				
Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile
	130				135					140					
Val	Ile	Ser	Ile	Asp	Tyr	Trp	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu
145				150					155					160	
Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys
			165					170					175		
Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys
		180				185					190				
Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Met	Ala
	195					200					205				
Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser
	210				215					220					
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Val	Lys	Ile	Cys	Val	Phe	Ile
225				230					235					240	
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu
			245					250						255	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu
		260				265					270				
Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val
	275					280					285				
Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile
	290				295					300					
Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp
305				310					315					320	
His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val
			325					330						335	
Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Glu	Phe
		340				345					350				
Cys	Ile	Pro	Thr	Ser	Ser	As									

SEQ ID NO:3

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61 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggctgag gcgcttgga cccgaaaagt ctggtgctc ctggtacct
181 cgcacagcgg tgcccgcccg gccgtcagta ccatggacag cagcgtgcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgtag caagttggc cccagcacc agccccgggt
301 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcggt ccgaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtcctctc atgatcacgg
421 ccatacagat catggccctc tactccatcg tgtgcgtggg ggggctcttc ggaaacttcc
481 tggatcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtaccct gcccttcag agtgtgaatt
601 acctaatggg aacatggcca ttggaacca tcctttgcaa gatagtgat tccatagatt
661 actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacatgt
721 cagtctgcc cctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaa ctggatcctc tcttcagcca ttggtcttcc tgtaatgttc atggctacaa
841 caaaatacag gcaagggttc atagattgta cactaacatt ctctcatcca acctgggtact
901 gggaaaacct cgtgaagatc tgtgttttca tcttcgctt cattatgcca gtgctcatca
961 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcatg ctctctggct
1021 ccaaagaaaa ggacaggaat ctccgaagga tcaccaggat ggtgctgggt gtgggtggctg
1081 tgttcacgt ctgctggact cccattcaca tttagctcat cattaaagcc ttggttacaa
1141 tcccagaaac tacgttcag actgtttctt ggcacttctg cattgtctta ggttacacaa
1201 acagctgcct caacccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1261 gagagttctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaactactag agaccacccc tccacggcca atacagtga tagaactaat catcagctag
1381 aaaatctgga agcagaaact gctccgttgc cctaacaggg tctcatgcca ttccgacctt
1441 caccaagctt agaagccacc atgtatgtgg aagcagggtt cttcaagaat gtgtaggagg
1501 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
1561 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttgga aggaaaggaa
1621 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaccaa acccatcgtg
1681 gtatgtgaat tgaagtcac ataaaagggt acccttctgt ctgtaagatt ttattttcaa
1741 gcaaatattt atgacctcaa caaagaagaa ccatcttttg ttaagttcac cgtagtaaca
1801 cataaagtaa atgctacctc tgatcaaagc accttgaatg gaaggctcga gtctttttag
1861 tgtttttgca agggaaatgaa tccattatc tatttttagac ttttaacttc aacttaaaat
1921 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1981 aataacatct ctttcatcta gctccataat tgcaagggaa gagattagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaataactt
2101 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtgggttg ttcctggaat
2161 tc

T00130-6000000

600-1-266P FIGURE 2B

SEQ ID NO:4

Met	Asp	Ser	Ser	Ala	Ala	Pro	Thr	Asn	Ala	Ser	Asn	Cys	Thr	Asp	Ala
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Leu	Ala	Tyr	Ser	Ser	Cys	<u>Pro</u>	Pro	Ala	Pro	Ser	Pro	Gly	Ser	Trp	Val
			20				25						30		
Asn	Leu	Ser	His	Leu	Asp	Gly	Asn	Leu	Ser	Asp	Pro	Cys	Gly	Pro	Asn
		35					40					45			
Arg	Thr	Asn	Leu	Gly	Gly	Arg	Asp	Ser	Leu	Cys	Pro	Pro	Thr	Gly	Ser
	50					55					60				
Pro	Ser	Met	Ile	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val
	65				70					75				80	
Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val
			85						90					95	
Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu
			100					105					110		
Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val
	115						120					125			
Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile
	130					135					140				
Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu
	145				150					155				160	
Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys
			165					170						175	
Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys
		180						185					190		
Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Met	Ala
		195				200						205			
Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser
	210					215					220				
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Val	Lys	Ile	Cys	Val	Phe	Ile
	225				230					235				240	
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu
			245					250						255	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu
		260						265					270		
Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val
		275					280					285			
Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile
	290					295					300				
Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp
	305				310					315				320	
His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val
			325					330						335	
Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Glu	Phe
		340						345					350		
Cys	Ile	Pro	Thr	Ser	Ser	Asn	Ile	Glu	Gln	Gln	Asn	Ser	Thr	Arg	Ile
		355					360					365			
Arg	Gln	Asn	Thr	Arg	Asp	His	Pro	Ser	Thr	Ala	Asn	Thr	Val	Asp	Arg
	370					375					380				
Thr	Asn	His	Gln	Leu	Glu	Asn	Leu	Glu	Ala	Glu	Thr	Ala	Pro	Leu	Pro
	385				390					395					400

600-1-266P

SEQ ID NO:5

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga
61 cgctccctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggctgag gcgcttggaa cccgaaaagt ctcggtgctc ctggctacct
181 cgcacagcgg tgcccggccg gccgtcagta ccatggacag cagcgtgcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgtact caagttgctc cccagcacc agccccgggt
301 cctgggtcaa cttgtccac ttagatggca acctgaccga cccatgcggg ccgaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtcctctc atgatcacgg
421 ccatcacgat catggccctc tactccatcg tgtgcgtggg ggggctcttc ggaaacttcc
481 tggcatgtga tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtaccct gcccttccag agtgtgaatt
601 acctaatggg aacatggcca tttggaacca tcctttgcaa gatagtgat tccatagatt
661 actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacattg
721 cagtctgcca cctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaa ctggatcctc tcttcagcca ttggtcttcc tgtaatgttc atggctacaa
841 caaaatacag gcaaggttcc atagattgta cactaacatt ctctcatcca acctgggtact
901 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgtcatca
961 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcatg ctctctggct
1021 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctggtg gtggtggctg
1081 tgttcatcgt ctgctggact cccattcaca tttacgtcat cattaagcc ttggttacaa
1141 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgctcta ggttacacaa
1201 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1261 gagagtcttg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaacactag agaccacccc tccacggcca atacagtga tagaactaat catcagctag
1381 aaaatctgga agcagaaact gctccgttgc cctaacaggg tctcatgcca ttccgacctt
1441 caccaagctt agaagccacc atgtatgtgg aagcaggttg cttcaagaat gtgtaggagg
1501 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
1561 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttgga aggaaaggaa
1621 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaccaa acccatcgtg
1681 gtatgtgaat tgaagtcac ataaaagggtg acccttctgt ctgtaagatt ttattttcaa
1741 gcaaatatth atgacctcaa caaagaagaa ccacttttg ttaagttcac cgtagtaaca
1801 cataaagtaa atgctacctc tgatcaaagc accttgaatg gaaggccga gtctttttag
1861 tgtttttgca agggaatgaa tccattatc tattttagac ttttaacttc aacttaaaat
1921 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1981 aataacatct ctttcatcta gctccataat tgcaaggga gagattagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaatactt
2101 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtggtttg ttcttggaa
2161 tc

600-1-266P-051301

600-1-266P

FIGURE 3B

SEQ ID NO:6

Met	Asp	Ser	Ser	Ala	Ala	Pro	Thr	Asn	Ala	Ser	Asn	Cys	Thr	Asp	Ala
1				5					10					15	
Leu	Ala	Tyr	Ser	Ser	Cys	Ser	Pro	Ala	Pro	Ser	Pro	Gly	Ser	Trp	Val
			20					25					30		
Asn	Leu	Ser	His	Leu	Asp	Gly	Asn	Leu	<u>Thr</u>	Asp	Pro	Cys	Gly	Pro	Asn
		35					40					45			
Arg	Thr	Asn	Leu	Gly	Gly	Arg	Asp	Ser	Leu	Cys	Pro	Pro	Thr	Gly	Ser
	50					55					60				
Pro	Ser	Met	Ile	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val
	65				70					75				80	
Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val
				85					90					95	
Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu
			100					105					110		
Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val
		115					120					125			
Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile
	130					135					140				
Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu
	145				150				155					160	
Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys
				165					170					175	
Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys
			180					185					190		
Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Met	Ala
		195					200					205			
Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser
	210					215					220				
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Val	Lys	Ile	Cys	Val	Phe	Ile
	225				230					235				240	
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu
				245					250					255	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu
		260						265					270		
Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val
		275					280					285			
Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile
	290					295						300			
Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp
	305				310					315				320	
His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val
				325					330					335	
Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Glu	Phe
			340					345				350			
Cys	Ile	Pro	Thr	Ser	Ser	Asn	Ile	Glu	Gln	Gln	Asn	Ser	Thr	Arg	Ile
		355					360					365			
Arg	Gln	Asn	Thr	Arg	Asp	His	Pro	Ser	Thr	Ala	Asn	Thr	Val	Asp	Arg
	370					375					380				
Thr	Asn	His	Gln	Leu	Glu	Asn	Leu	Glu	Ala	Glu	Thr	Ala	Pro	Leu	Pro
	385				390					395				400	

T08T90 6666660

SEQ ID NO:7

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1  ggaattccgg ctataggcag aggagaatgt cagatgctca gtcggtccc ctccgcctga
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121  ggcgaaagga agcggtgag gcgcttgga cccgaaaagt ctcggtgctc ctggctacct
181  cgcacagcgg tgcgcgcgc gccgtcagta ccatggacag cagcgctgcc cccacgaacg
241  ccagcaattg cactgatgcc ttggcgctac caagtgtctc cccagcacc agccccgggt
301  cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcggt ccgaaccgca
361  ccaatctggg cgggagagac agcctgtgcc ctccgaccgg cagtcctctc atgatcacgg
421  ccatcacgat catggccctc tactccatcg tgtgcgtggg ggggctcttc ggaaacttcc
481  tggatcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
541  tcaacttgtc tctggcagat gccttagcca ccagtacct gcccttcag agtgtgaatt
601  acctaatggg aacatggcca tttggaacca tcctttgcaa gatagtgat tccatagatt
661  actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacattg
721  cagtctgcc cctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781  atgtctgcaa ctggatcctc tcttcagcca ttggtcttcc tgtaatgttc atggctacaa
841  caaaatacag gcaaggttcc atagattgta cactaacatt ctctcatcca acctggtact
901  gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgctcatca
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1081  tgttcatcgt ctgctggact cccattcaca tttacgtcat cattaagcc ttggttacaa
1141  tcccagaaac tacgttccag actgtttctt ggcacttctg cattgctcta ggttacacaa
1201  acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaa cgatgcttca
1261  gagagttctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1321  agaactag agaccacccc tccacggcca atacagtga tagaactaat catcagctag
1381  aaaatctgga agcagaaact gtcggttgc cctaacaggg tctcatgcca tccgacctt
1441  caccaagctt agaagccacc atgtatgtgg aagcaggtt cttcaagaat gtgtaggagg
1501  ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
1561  ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttgga aggaaggaa
1621  tataccacac cgaggagtcc agtttgtgca agacaccag tggaaacaaa acccatcgtg
1681  gtatgtgaat tgaagtcac ataaaagggt acccttctgt ctgtaagatt ttattttcaa
1741  gcaaatattt atgacctcaa caaagaagaa ccatcttttg ttaagtccac cgtagtaaca
1801  cataaagtaa atgctacctc tgatcaaagc acctgaatg gaaggccga gtcttttag
1861  tgtttttgca agggaatgaa tccattattc tattttagac ttttaacttc aacttaaaat
1921  tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1981  aataacatct ctttcatcta gctccataat tgcaaggga gagattagca tgaaaggtaa
2041  tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaatactt
2101  ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtgggttg ttcctggaat
2161  tc

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600-1-266P "GE3E3360"

SEQ ID NO:8

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggctgag gcgcttgaa cccgaaaagt ctcggtgctc ctgggtacct
181 cgcacagcgg tgcccggccg gccgtcagta ccatggacag cagcgtgcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgta ct caagttgctc cccagcacc agccccggtt
301 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcggt cccaaccgca
361 ccaacctggg cgggagagac agcctatgcc ctccgaccgg cagtccctcc atgatcacgg
421 ccatcacgat catggccctc tactccatcg tgtgcgtggg ggggctcttc ggaaacttcc
481 tggcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtaacct gcccttccag agtgtgaatt
601 acctaatggg aacatggcca tttggaacca tcttttgcaa gatagtgate tccatagatt
661 actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacattg
721 cagtctgcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaa ctggatcctc tcttcagcca ttggtcttcc tgtaatgttc atggctacaa
841 caaaatacag gcaagggttc atagattgta caactaacatt ctctcatcca acctggtact
901 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgctcatca
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1021 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctggtg gtggtggctg
1081 tgttcatcgt ctgctggact ccattcaca ttacgtcat cattaaagcc ttggtacaa
1141 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgctcta ggttacaaa
1201 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1261 gagagtctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaacactag agaccacccc tccacggcca atacagtga tagaactaat catcagctag
1381 aaaatctgga agcagaaact gtcctgttgc cctaacaggg tctcatgcca ttcggacctt
1441 caccaagctt agaagccacc atgtatgtgg aagcagggtt cttcaagaat gtgtaggagg
1501 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
1561 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttgga aggaaaggaa
1621 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaacaaa acccatcgtg
1681 gtatgtgaat tgaagtcac ataaaagggt acccttctgt ctgtaagatt ttattttcaa
1741 gcaaatattt atgacctcaa caaagaagaa ccatcttttg ttaagttcac cgtagtaaca
1801 cataaagtaa atgctacctc tgatcaaagc acctgaatg gaaggctcga gtctttttag
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1921 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1981 aataacatct ctttcatcta gctccataat tgcaaggga gagattagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaataactt
2101 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtgggttg ttcttggaa
2161 tc

093339-061001

SEQ ID NO:9

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcgggtgag gcgcttgga cccgaaaagt ctcgggtgctc ctgggtacct
181 cgacacagcg tgcccgccc gccgtcagta ccatggacag cagcgtgccc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgact caagttgctc cccagcacc agccccggtt
301 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcggt ccgaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg **cgccagtcctcc** atgatcacgg
424 ccatcacgat catggccctc tactccatcg tgtgcgtggt ggggctcttc ggaaacttcc
484 tggtcattgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
544 tcaaccttgc tctggcagat gccttagcca ccagtaccct gcccttccag agtgtgaatt
604 acctaatggg aacatggcca tttggaacca tcttttgcaa gatagtgatc tccatagatt
664 actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacattg
724 cagtctgcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
784 atgtctgcaa ctggatcctc tcttcagcca ttggtcttcc tgtaatgttc atgggtacaa
844 caaaatacac gcaaggttcc atagattgta cactaacatt ctctcatcca acctggtact
904 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgctcatca
964 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcag ctctctggct
1024 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctgggt gtgggtggctg
1084 tgttcacgtg ctgctggact cccattcaca ttacgctcat cattaaagcc ttggtacaaa
1144 tcccagaaac tacgttccag actgtttctt ggcaacttctg cattgctcta gggttacaaa
1204 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1264 gagagttctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1324 agaacactag agaccacccc tccacggcca atacagtga tagaactaat catcagctag
1384 aaaatctgga agcagaaact gctccgttgc cctaacaggg tctcatgcca ttccgacctt
1444 caccaagctt agaagccacc atgtatgtgg aagcaggttg cttaagaat gtgtaggagg
1504 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
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1624 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaccaa acccatcgtg
1684 gtatgtgaat tgaagtcac ataaaagggt acccttctgt ctgtaagatt ttattttcaa
1744 gcaaatattt atgacctcaa caaagaagaa ccatcttttg ttaagttcac cgtagtaaca
1804 cataaagtaa atgctacctc tgatcaaagc accttgaatg gaaggtcga gtcttttag
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1924 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1984 aataacatct ctttcatcta gctccataat tgcaaggga gagattagca tgaaaggtaa
2044 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaatactt
2104 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtggtttg ttcttggaa
2164 tc

109839.06.1801

600-1-266P FIGURE 6B

SEQ ID NO:10

Met	Asp	Ser	Ser	Ala	Ala	Pro	Thr	Asn	Ala	Ser	Asn	Cys	Thr	Asp	Ala
1				5					10					15	
Leu	Ala	Tyr	Ser	Ser	Cys	Ser	Pro	Ala	Pro	Ser	Pro	Gly	Ser	Trp	Val
			20					25					30		
Asn	Leu	Ser	His	Leu	Asp	Gly	Asn	Leu	Ser	Asp	Pro	Cys	Gly	Pro	Asn
		35					40					45			
Arg	Thr	Asn	Leu	Gly	Gly	Arg	Asp	Ser	Leu	Cys	Pro	Pro	Thr	Gly	<u>Gly</u> Ser
	50					55					60				
Pro	Ser	Met	Ile	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val
66				71						76				81	
Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val
				86					91					96	
Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu
			101					106					111		
Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val
			116				121					126			
Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile
	131					136					141				
Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu
146					151					156					161
Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys
				166					171					176	
Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys
			181					186					191		
Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Met	Ala
		196				201						206			
Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser
	211					216					221				
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Val	Lys	Ile	Cys	Val	Phe	Ile
226					231					236					241
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu
				246					251					256	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu
			261					266					271		
Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val
		276					281					286			
Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile
		291				296					301				
Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp
306					311					316					321
His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val
				326					331					336	
Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Glu	Phe
			341					346					351		
Cys	Ile	Pro	Thr	Ser	Ser	Asn	Ile	Glu	Gln	Gln	Asn	Ser	Thr	Arg	Ile
		356					361					366			
Arg	Gln	Asn	Thr	Arg	Asp	His	Pro	Ser	Thr	Ala	Asn	Thr	Val	Asp	Arg
	371					376					381				
Thr	Asn	His	Gln	Leu	Glu	Asn	Leu	Glu	Ala	Glu	Thr	Ala	Pro	Leu	Pro
386					391					396					401

0583339.064804

6 0-1-266P FIG 7A







